

SEQUENCE LISTING

<110> BROUN, Pierre
VAN DE LOO, Frank
BODDUPALLI, Sekhar
SOMERVILLE, Chris

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY
MODIFIED PLANTS

<130> 20263/255164

<140> 09/117,921

<141> 1999-03-04

<150> 08/597,313

<151> 1996-02-06

<150> PCT/US97/02187

<151> 1997-02-06

<160> 15

<170> MS Word

<210> 1

<211> 543

<212> DNA

<213> *Lesquerella fendleri*

<220>

<221> UNSURE

<222> 83

<223> any

<400> 1

tattggcacc	ggcggcacca	ttccaacaat	ggatccctag	aaaaagatga	agtctttgtc	60
ccacctaa	aagctgcagt	canatgggtat	gtcaaatacc	tcaacaaccc	tcttgggacgc	120
attctgggtg	taacagttca	gtttatcctc	gggtggccct	tgtatctagc	ctttaatgta	180
tcaggtagac	cttatgatgg	tttcgcttca	catttcttcc	ctcatgcacc	tatctttaag	240
gaccgtgaac	gtctccagat	atacatctca	gatgctggta	ttctagctgt	ctggttatggt	300
ctttaccggt	acgctgcttc	acaaggattg	actgctatga	tctgcgtcta	cggagtaccg	360
cttttgatag	tgaacttttt	ccttgccttg	gtcactttct	tgcagcacac	tcctccttca	420
ttacctcact	atgattcaac	cgagtgggaa	tggattagag	gagctttggt	tacggtagac	480
agagactatg	gaatcttgaa	caagggtgtt	cacaacataa	cagacacca	cgtagcacac	540
cac						543

<210> 2

<211> 544

<212> DNA

<213> *Lesquerella fendleri*

<400> 2

tataggcacc	ggaggcacca	ttccaacaca	ggatccctcg	aaagagatga	agtattttgtc	60
ccaaagcaga	aatccgcaat	caagtgggtac	ggcgaatacc	tcaacaaccc	tcctgggtcgc	120
atcatgatgt	taactgtcca	gttcgtcctc	ggatggccct	tgtacttagc	cttcaacggt	180
tctggcagac	cctacaatgg	tttcgcttcc	catttcttcc	ccaatgctcc	tatctacaac	240
gaccgtgaac	gcctccagat	ttacatctct	gatgctggta	ttctagccgt	ctggttatggt	300
ctttaccggt	acgctgttgc	acaaggacta	gcctcaatga	tctgtctaaa	cggagtcccg	360
cttctgatag	ttaacttttt	cctcgtcctg	atcacttact	tacaacacac	tcaccctgcg	420

ttgcctcact atgattcatc agagtgggat tggcttagag gagctttage tactgtagac 480
 agagactatg gaatcttgaa caaggtgttc cataacatca cagacacca cgctgcacac 540
 cact 544

<210> 3
 <211> 1855
 <212> DNA
 <213> *Lesquerella fendleri*

<220>
 <221> UNSURE
 <222> 46, 99, 203, 1658, 1788
 <223> any

<400> 3
 atgaagcttt ataagaagtt agttttctct ggtgacagag aaattntgtc aattggtagt 60
 gacagttgaa gcaacaggaa caacaaggat gggtgggtgnt gatgctgatg tgggtgatgtg 120
 ttattcatca aataactaaat actacattac ttgttgctgc ctacttctcc tatttcctcc 180
 gccaccatt ttggaccac ganccttcca tttaaacct ctctcgtgct attcaccaga 240
 agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcacgtgta 300
 ttaacgtaag ttttttttga ccactcatat ctaaaatcta gtacatgcaa tagattaatg 360
 actgttcctt cttttgatat tttcagcttc ttgaattcaa gatgggtgct ggtggaagaa 420
 taatggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480
 agaaaccacc attcactggt aaagatctga agaaagcaat cccacagcat tgtttcaagc 540
 gctctatccc tegtctcttc tctaccttc tcacagatat cacttttagt tcttgcttct 600
 actacgttgc cacaaattac ttctctcttc tctctcagcc tctctctact tacctagctt 660
 ggctctcta ttgggtatgt caaggctgtg tcttaaccgg tatctgggtc attggccatg 720
 aatgtgggtca ccatgcattc agtgactatc aatgggtaga tgacactgtt ggttttatct 780
 tccattcctt ccttctcgtc ccttacttct cctggaaata cagtcacgt cgtcaccatt 840
 ccaacaatgg atctctcgag aaagatgaag tctttgtccc accgaagaaa gctgcagtca 900
 aatgggtatgt taaataacct aacaaccctc ttggacgcat tctgggtgta acagttcagt 960
 ttatcctcgg gtggcctttg tatctagcct ttaatgtatc aggtagacct tatgatggtt 1020
 tcgcttcaca tttcttccct catgcaccta tctttaaaga ccgagaacgc ctccagatat 1080
 acatctcaga tgctgggtatt ctagctgtct gttatggtct ttaccgttac gctgcttcac 1140
 aaggattgac tgctatgac tgctctatg gagtaccgct tttgatagtg aacttttctc 1200
 ttgtcttgggt aactttcttg cagcacactc atcctcgtt acctcattat gattcaaccg 1260
 agtgggaatg gattagagga gctttgggtta cggtagacag agactatgga atattgaaca 1320
 aggtgttcca taacataaca gacacacatg tggctcatca tctctttgca actataccgc 1380
 attataacgc aatggaagct acagaggcga taaagccaat acttggtgat tactaccact 1440
 tcgatggaac accgtggtat gtggccatgt ataggggaagc aaaggagtgt ctctatgtag 1500
 aaccggatag ggaacgtggg aagaaggtg tctactatta caacaataag ttatgaggct 1560
 gatagggcga gagaagtgc attatcaatc ttcatttcca tgttttaggt gtcttggtta 1620
 agaagctatg ctttggttca ataatctcag agtccatnta gttgtgttct ggtgcatttt 1680
 gcctagttat gtgggtgcgg aagttagtgt tcaaaactgct tctgctgtg ctgcccagt 1740
 aagaacaagt ttacgtgttt aaaatactcg gaacgaattg accacaanat atccaaaacc 1800
 ggctatccga attccatata cgaaaaccgg atatccaaat ttccagagta cttag 1855

<210> 4
 <211> 384
 <212> PRT
 <213> *Lesquerella fendleri*

<400> 4
 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
 1 5 10 15
 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
 20 25 30

Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
 35 40 45
 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65 70 75 80
 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
 85 90 95
 Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
 100 105 110
 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
 115 120 125
 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
 130 135 140
 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
 145 150 155 160
 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
 165 170 175
 Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
 180 185 190
 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
 195 200 205
 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
 210 215 220
 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240
 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
 245 250 255
 Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
 260 265 270
 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
 275 280 285
 Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300
 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320
 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
 325 330 335
 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
 340 345 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
 355 360 365

Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
 370 375 380

<210> 5

<211> 387

<212> PRT

<213> Ricinus communis

<400> 5

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
 1 5 10 15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
 20 25 30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
 35 40 45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
 50 55 60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
 65 70 75 80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
 85 90 95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
 100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
 115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
 130 135 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
 145 150 155 160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
 165 170 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
 180 185 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 195 200 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
 210 215 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
 225 230 235 240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
 245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
 260 265 270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
 275 280 285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
 290 295 300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
 305 310 315 320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
 325 330 335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
 340 345 350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
 355 360 365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
 370 375 380

Asn Lys Tyr
 385

<210> 6

<211> 383

<212> PRT

<213> Arabidopsis thaliana

<400> 6

Met Gly Ala Gly Gly Arg Met Pro Val Pro Thr Ser Ser Lys Lys Ser
 1 5 10 15

Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
 20 25 30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
 50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
 65 70 75 80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
 100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
 145 150 155 160
 Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
 165 170 175
 Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
 180 185 190
 Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
 195 200 205
 His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
 210 215 220
 Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr
 225 230 235 240
 Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly
 245 250 255
 Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu
 260 265 270
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 275 280 285
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300
 Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 305 310 315 320
 Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile
 325 330 335
 Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr
 340 345 350
 Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
 355 360 365
 Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 7
 <211> 383
 <212> PRT
 <213> Brassica napus

<400> 7
 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
 1 5 10 15
 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
 20 25 30
 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
 35 40 45

Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser
 50 55 60
 Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro
 65 70 75 80
 Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
 85 90 95
 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe
 100 105 110
 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
 115 120 125
 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
 130 135 140
 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg
 145 150 155 160
 Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly
 165 170 175
 Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr
 180 185 190
 Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys
 195 200 205
 His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln
 210 215 220
 Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu
 225 230 235 240
 Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg
 245 250 255
 Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
 260 265 270
 Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
 275 280 285
 Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 290 295 300
 Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu
 305 310 315 320
 Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
 325 330 335
 Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val
 340 345 350
 Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
 355 360 365

Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
 370 375 380

<210> 8
 <211> 309
 <212> PRT
 <213> Glycine max

<400> 8
 Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp Leu Ser Phe Ala
 1 5 10 15

Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Gln Pro
 20 25 30

Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu
 35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val
 50 55 60

Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr
 65 70 75 80

Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser
 85 90 95

Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu
 100 105 110

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
 115 120 125

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
 130 135 140

Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr
 145 150 155 160

Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val
 165 170 175

Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro
 180 185 190

Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val
 195 200 205

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr
 210 215 220

Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr
 225 230 235 240

Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His
 245 250 255

Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr
 260 265 270

Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val
 275 280 285

Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn
 290 295 300

Lys Tyr Leu Arg Val
 305

<210> 9
 <211> 302
 <212> PRT
 <213> Glycine max

<400> 9
 Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe Cys Leu Tyr Tyr
 1 5 10 15

Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro Leu Ser Phe Arg
 20 25 30

Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val
 35 40 45

Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly
 50 55 60

Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr
 65 70 75 80

Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu
 85 90 95

Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg
 100 105 110

Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu
 115 120 125

Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr
 130 135 140

Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu
 145 150 155 160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
 165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
 180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
 195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
 210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
 225 230 235 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr
 245 250 255
 Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala
 260 265 270
 Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly
 275 280 285
 Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val
 290 295 300

<210> 10
 <211> 371
 <212> PRT
 <213> Zea mays

<400> 10

Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu
 1 5 10 15
 Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val
 20 25 30
 Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro
 35 40 45
 His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His
 50 55 60
 Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile
 65 70 75 80
 Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp
 85 90 95
 Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val
 100 105 110
 Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys
 115 120 125
 Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp
 130 135 140
 Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro
 145 150 155 160
 Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln
 165 170 175
 Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg
 180 185 190
 Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr
 195 200 205
 Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val
 210 215 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
 225 230 235 240
 Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
 245 250 255
 Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
 260 265 270
 Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
 275 280 285
 Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
 290 295 300
 Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
 305 310 315 320
 Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
 325 330 335
 Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
 340 345 350
 Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
 355 360 365
 Lys Lys Phe
 370

<210> 11
 <211> 224
 <212> PRT
 <213> Ricinus communis

<400> 11
 Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
 1 5 10 15
 Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val
 20 25 30
 Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
 35 40 45
 Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
 50 55 60
 Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
 65 70 75 80
 Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
 85 90 95
 Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
 100 105 110
 Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
 115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile
 130 135 140
 Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
 145 150 155 160
 Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
 165 170 175
 Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
 180 185 190
 Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
 195 200 205
 His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
 210 215 220

<210> 12
 <211> 20
 <212> DNA
 <213> Ricinus communis

<400> 12
 gctcttttgt gcgctcattc 20

<210> 13
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: homologous
 regions of Ricinus communis deduced by hydroxylase
 sequence and Arabidopsis thaliana deduced desaturase
 sequence for use as oligonucleotide primer

<400> 13
 cggtaccaga aaacgccttg 20

<210> 14
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: homologous
 regions of Ricinus communis deduced by hydroxylase
 sequence and Arabidopsis thaliana deduced
 desaturase sequence for use as oligonucleotide primer

<220>
 <221> UNSURE
 <222> 6, 12, 15
 <223> any

<400> 14
 taywsncaym gnmgnca yca 20

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: homologous
regions of Ricinus communis deduced by hydroxylase
sequence and Arabidopsis thaliana deduced
desaturase sequence for use as oligonucleotide primer

<220>
<221> UNSURE
<222> 7, 10, 16
<223> any

<400> 15
rtgrtgngcn acrtgngtrt c

21